UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, D.C. 20231
www.uspto.gov

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/873,881	06/04/2001	Fred W. Scott	18617.NEW

CONFIRMATION NO. 6373
FORMALITIES LETTER

OC000000007141372

Ranjana Kadle
Hodgson Russ LLP
Suite 2000
One M&T Plaza
Buffalo, NY 14203-2391

Date Mailed: 11/30/2001

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

**For questions regarding compliance to these requirements, please contact:**

- **For Rules Interpretation, call (703) 308-4216**
- **To Purchase PatentIn Software, call (703) 306-2600**
- **For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov**

A copy of this notice MUST be returned with the reply.

Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 3 - OFFICE COPY

RAW SEQUENCE LISTING ERROR REPORT

BIOTEC ОLOGY SYSTEMS BRANCH
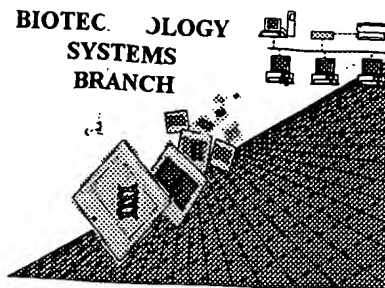
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/873,881A*

Source: *OIPE*

Date Processed by STIC: *10/15/2001*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING   DATE: 10/15/2001
PATENT APPLICATION: US/09/873,881A   TIME: 15:47:14

Input Set : **A:\corrected sequence listing for Scott et al**
Output Set: **N:\CRF3\10152001\I873881A.raw**

```
   3 <110> APPLICANT: Scott, Fred W.
   5 <120> TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
   7 <130> FILE REFERENCE: 18617.0016
   9 <140> CURRENT APPLICATION NUMBER: US 09/873,881A
  10 <141> CURRENT FILING DATE: 2001-06-04
  12 <150> PRIOR APPLICATION NUMBER: US 08/552,369
  13 <151> PRIOR FILING DATE: 1995-11-03
  15 <160> NUMBER OF SEQ ID NOS: 19
```

Does Not Comply
Corrected Diskette Needed

pp 1,3-4

ERRORED SEQUENCES

```
 932 <210> SEQ ID NO: 19
 933 <211> LENGTH: 1979
 934 <212> TYPE: DNA
 935 <213> ORGANISM: feline leukemia virus
 937 <220> FEATURE:
 938 <223> OTHER INFORMATION:
 940 <400> SEQUENCE: 19
 941 accaccaatc aagacctctc ggacagcccc agctcagacg atccatcaag       50
 943 atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc    95
 944 Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu
 945  1               5                   10                  15
 947 tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac   140
 948 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp
 949              20                  25                  30
 951 ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act   185
 952 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr
 953              35                  40                  45
 955 tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc   230
 956 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr
 957              50                  55                  60
 959 tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt   275
 960 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val
 961              65                  70                  75
 963 gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta   320
 964 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu
 965                  80                  85                  90
 967 aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa   365
 968 Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys
W--> 969              95                  100                 105
 971 tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac   410
 972 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr
(W--) 973              110                 115                 120
 975 ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag   455
 976 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys
W--> 977              125                 130                 135
```

delete

OK

*--> numbers are
in bold print
--> due to error
above - apostrophe*

RAW SEQUENCE LISTING   DATE: 10/15/2001
PATENT APPLICATION: US/09/873,881A   TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al
Output Set: N:\CRF3\10152001\I873881A.raw

```
       979 gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg    500
       980 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
W--> 981              140                 145                 150
       983 gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca    545
       984 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser
W--> 985              155                 160                 165
       987 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc    590
       988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser
W--> 989              170                 175                 180
       991 tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag    635
       992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys
W--> 993              185                 190                 195
       995 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga    680
       996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg
W--> 997              200                 205                 210
       999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc    725
      1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser
W--> 1001             215                 220                 225
      1003 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac    770
      1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
W--> 1005             230                 235                 240
      1007 cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca    815
      1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr
W--> 1009             245                 250                 255
      1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc    860
      1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala
W--> 1013             260                 265                 270
      1015 cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg    905
      1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly
W--> 1017             275                 280                 285
      1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc    950
      1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala
W--> 1021             290                 295                 300
      1023 tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc    995
      1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys
W--> 1025             305                 310                 315
      1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt   1040
      1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly
W--> 1029             320                 325                 330
      1031 acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act   1085
      1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile
W--> 1033             335                 340                 345
      1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg   1130
      1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met
W--> 1037             350                 355                 360
      1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag   1175
      1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys
W--> 1041             365                 370                 375
      1043 aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac   1220
```

RAW SEQUENCE LISTING   DATE: 10/15/2001
PATENT APPLICATION: US/09/873,881A   TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al
Output Set: N:\CRF3\10152001\I873881A.raw

```
        1044 Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn
W--> 1045             380             385             390
        1047 ggc acc tat tgg gcc tgt aac act gga ctc acc cca tgc att tcc  1265
        1048 Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser
W--> 1049             395             400             405
        1051 atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa  1310
        1052 Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu
W--> 1053             410             415             420
        1055 tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca  1355
        1056 Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
W--> 1057             425             430             435
        1059 cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta  1400
        1060 His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile Ser Leu
W--> 1061             440             445             450
        1063 acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc  1445
        1064 Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
W--> 1065             455             460             465
        1067 gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag  1490
        1068 Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
W--> 1069             470             475             480
        1071 ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta  1535
        1072 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
W--> 1073             485             490             495
        1075 gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct  1580
        1076 Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
W--> 1077             500             505             510
        1079 gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta  1625
        1080 Glu Val Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu
W--> 1081             515             520             525
        1083 caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc  1670
        1084 Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
W--> 1085             530             535             540
        1087 tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta  1715
        1088 Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
W--> 1089             545             550             555
        1091 aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag  1760
        1092 Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
W--> 1093             560             565             570
        1095 gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc  1805
        1096 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
W--> 1097             575             580             585
        1099 cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att  1850
        1100 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Leu Ile
W--> 1101             590             595             600
        1103 ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta  1895
        1104 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe Val
W--> 1105             605             610             615
        1107 aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag  1940
W--> 1108 Lys Asp Arg Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln Gln
```

```
W--> 1109              620            625            630
     1111 tac caa cag ata aag caa tac gat ccg gac cga cca tga      1979
     1112 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
W--> 1113              635            640
E--> 1117  bFLOdOcs:589477_1 (cm%d01)
```

delete

VERIFICATION SUMMARY   DATE: 10/15/2001
PATENT APPLICATION: US/09/873,881A   TIME: 15:47:16

Input Set : A:\corrected sequence listing for Scott et al
Output Set: N:\CRF3\10152001\I873881A.raw

L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:912 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:989 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:993 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:997 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1001 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1995 SEQ:19
L:1117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
L:1117 M:112 C: (48) String data converted to lower case,
L:1117 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1979 Found:1995 SEQ:19